INFORMATION DISCLOSURE STATEMENT	Atty. Docket No.: 6315.N	Serial No.: 09/772,598
	Applicant(s): T. Benson et al.	Confirmation No.: 2967
	Filing Date: January 30, 2001	Group: 2183

U.S. PATENT DOCUMENTS

Examiner Initial		Document Number	Date	Name	Class	Subclass	Filing Date If Appropriate
		none					

FOREIGN PATENT DOCUMENTS

Examiner Initial		Document Number	Date	Country	Class	Subclass	Translation Yes	Translation No
CSM	✓	WO 93/02209 A1	02/04/93	PCT				
	✓	WO 97/15588 A1	05/01/97	PCT				
	✓	EP 0786 519 A2	07/30/97	Europe				
	✓	WO 98/58961 A1	12/30/98	PCT				
	✓	WO 99/36422 A1	07/22/99	PCT				
	✓	WO 99/47639 A2	09/23/99	PCT				
	✓	WO 99/47662 A1	09/23/99	PCT				
	✓	WO 00/12678 A2	03/09/00	PCT				
	✓	WO 00/12678 A3	03/09/00	PCT				
	✓	WO 01/16292 A2	03/08/01	PCT				
↓								

OTHER DOCUMENTS (Including Authors, Title, Date, Pertinent Papers, etc.)

Examiner Initial		Document Description
CSM	✓	Bartlett et al., "CAVEAT: A program to facilitate the structure-derived design of biologically active molecules," *Molecular Recognition: Chemical and Biological Problems*, Royal Society of Chemistry, Special Pub No. 78:182-196 (1989).
	✓	Benson et al. "An enzyme-substrate complex involved in bacterial cell wall biosynthesis," *Nat Struct Biol.* 1995 Aug;2(8):644-53.
↓	✓	Blundell et al., *Protein Crystallography*, Academic Press, New York, NY; title page, publication page, and table of contents only, 8 pages (1976).

EXAMINER	Date Considered
C. Melt	September 16, 2002

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Examiner Initial		Document Description
		Böhm, "The computer program LUDI: a new method for the de novo design of enzyme inhibitors," *J. Comput. Aided Mol. Des.* 1992 Feb;6(1):61-78.
		Brünger, *X-plor Manual (Version 3.1) A System for X-ray Crystallography and NMR* (title page, publisher's page, and table of contents only), Yale University Press, New Haven, CT, 1992; 13 pgs.
		Collaborative Computational Project, No. 4, "The *CCP4* suite: programs for protein crystallography" *Acta Cryst.* 1994;*D50*:760-3.
		Cowtan et al., "Improvement of Macromolecular Electron-Density Maps by the Simultaneous Application of Real and Reciprocal Space Constraints," *Acta Crystallogr D Biol Crystallogr.* 1993 Jan 1;*49*(Pt 1):148-157.
		Cowtan et al., "Miscellaneous algorithms for density modification," *Acta Crystallogr D Biol Crystallogr.* 1998 Jul 1;*54*(Pt 4):487-93.
		Eisen et al., "HOOK: a program for finding novel molecular architectures that satisfy the chemical and steric requirements of a macromolecule binding site," *Proteins: Struct. Funct. Genet.* 1994 Jul;*19*(3):199-221.
		Evans, "SETOR: hardware-lighted three-dimensional solid model representations of macromolecules," *J Mol Graph.* 1993 Jun;11(2):134-8, 127-8.
		Finzel, "LORE: exploiting database of known structures," *Meth. Enzymol.* 1997; *277*(B):230-42.
		Gillet et al., "SPROUT: a program for structure generation," *J. Comput. Aided Mol. Des.* 1993 Apr;*7*(2):127-53.
		Goodford, "A computational procedure for determining energetically favorable binding sites on biologically important macromolecules," *J Med Chem.* 1985 Jul; *28*(7):849-57.
		Goodsell et al., "Automated docking of substrates to proteins by simulated annealing," *Proteins: Struct. Funct. Genet.* 1990;*8*(3):195-202.
		Hendrickson, "Determination of macromolecular structures from anomalous diffraction of synchrotron radiation," *Science.* 1991 Oct 4;*254*(5028):51-8.
		Hughes et al., "Structural gene for NAD synthetase in Salmonella typhimurium," *J Bacteriol.* 1988 May;170(5):2113-20.

EXAMINER C. Melb	Date Considered September 16, 2002

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Examiner Initial*		Document Description
✓		Jiang et al., "Protein hydration observed by X-ray diffraction. Solvation properties of penicillopepsin and neuraminidase crystal structures," *J. Mol. Biol.* 1994 Oct 14;*243*(1):100-15.
✓		Kraulis, "MOLSCRIPT: a program to produce both detailed and schematic plots of protein structures," *J. Appl. Cryst.* 1991 Oct;*24*:946-950.
✓		Kuntz et al., "A geometric approach to macromolecule-ligand interactions," *J. Mol. Biol.* 1982 Oct 25;*161*(2):269-88.
✓		Laemmli, "Cleavage of Structural Proteins during the Assembly of the Head of Bacteriophage T4," *Nature*, 1970 Aug 15;227(259):680-85.
✓		Laskowski, et al., "PROCHECK: a program to check the stereochemical quality of protein structures," *J. Appl Cryst.* 1993 Apr;*26*:283-291
✓		Lattman, "Use of the rotation and translation functions," *Methods Enzymol.* 1985;*115*:55-77.
✓		Lauri et al., "CAVEAT: a program to facilitate the design of organic molecules," *J Comput Aided Mol Des.* 1994 Feb;*8*(1):51-66.
✓		Martin, "3D database searching in drug design," *J. Med. Chem.* 1992 Jun 12; *35*(12):2145-54.
✓		Meng et al., "Automated docking with grid-based energy evaluation," *J. Comp. Chem*, 1992 May;*13*(4):505-524.
✓		Merritt et al., "*Raster3D* Version 2.0. A Program for Photorealistic Molecular Graphics", *Acta Crystallogr D Biol Crystallogr.*, 1994;*50*:869-73.
✓		Miranker et al., "Functionality maps of binding sites: a multiple copy simultaneous search method," *Proteins: Struct. Funct. Genet.* 1991;*11*(1):29-34.
✓		Moat et al., "Biosynthesis and salvage pathways of pyridine nucleotides. Coenzymes and cofactors, Pyridine Nucleotide Coenzymes," Eds. D. Dolphin et al. John Wiley & Sons, Inc., New York, 1987; vol.II, part B:1-24.
✓		National Institutes of Health, "BLAST 2 Sequences," [online] United States; retrieved October 15, 2001 from the Internet: <URL:http://www.ncbi.nlm.nih.gov/gorf/bl2.html>, 1 pg.
✓		Navaza, "AMoRe: an automated package for molecular replacement," *Acta Crystallogr A.* 1994 Mar;*50*:157-163.

EXAMINER C. Melf	Date Considered September 16, 2002

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Examiner Initial		Document Description
GSA	✓	Nessi et al., "The outB gene of *Bacillus subtilis* codes for NAD synthetase," *J Biol Chem*. 1995 Mar 17;270(11):6181-5.
	✓	Nishibata et al., "Automatic creation of drug candidate structures based on receptor structure. Starting point for artificial lead generation," *Tetrahedron*, 1991;*47*(43):8985-90.
	✓	Otwinowski, "Maximum likelihood refinement of heavy atom parameters," *Isomorphous replacement and anomalous scattering - Proceedings of the CCP4 Study Weekend 25-26 January 1991*, (W. Wolf et al., Eds.) Science and Engineering Research Counsel, Daresbury Laboratory, Warrington, U.K. (1991) pp. 80-86.
	✓	Ozment et al., "Structural study of Escherichia coli NAD synthetase: overexpression, purification, crystallization, and preliminary crystallographic analysis," *J. Struct. Biol.* 1999 Oct;*127*(3):279-82.
	✓	Ramakrishnan et al., "Crystal structure of globular domain of histone H5 and its implications for nucleosome binding," *Nature*. 1993 Mar 18;*362*(6417):219-23.
	✓	Research Collaboratory for Structural Bioinformatics, "Protein Data Bank," [online] United States; retrieved October 15, 2001 from the Internet: <URL: http://www.rcsb.org/pdb/> 1 page.
	✓	Rizzi et al., "Crystal structure of NH3-dependent NAD+ synthetase from Bacillus subtilis," *EMBO J.* 1996 Oct 1;*15*(19):5125-34.
	✓	Rizzi et al., "Crystallization of NAD+ synthetase from Bacillus subtilis," *Proteins*. 1996 Oct;26(2):236-8.
	✓	Rizzi et al., "A novel deamido-NAD+-binding site revealed by the trapped NAD-adenylate intermediate in the NAD+ synthetase structure," *Structure*. 1998 Sep 15;*6*(9):1129-40.
	✓	Rossmann et al., "Chemical and biological evolution of nucleotide-binding protein," *Nature*. 1974 Jul 19;*250*(463):194-9.
	✓	Rossmann, ed., *The Molecular Replacement Method - A Collection of Papers on the Use of Non-Crystallographic Symmetry*, *Intl. Sci. Rev. Ser. No. 13*, Gordon & Breach, New York, NY; title page, publication page, and table of contents only, 6 pages (1972).
✓	✓	Sack, "CHAIN - A Crystallographic Modeling Program," *J Molecular Graphics*. 1988 Dec; *6*(4):224-5.

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		Sheldrick et al., "Structure solution by iterative peaklist optimization and tangent expansion in space group P1," *Acta Crystallogr B.* 1995 Aug 1;51(Pt 4):423-31.
		Tatusova et al., "BLAST 2 Sequences, a new tool for comparing protein and nucleotide sequences," *FEMS Microbiol Lett.* 1999 May 15;*174*(2):247-50.
		Travis, "Proteins and organic solvents make an eye-opening mix," *Science.* 1993 Nov 26;*262*(5138):1374.
		Van Duyne et al., "Atomic structures of the human immunophilin FKBP-12 complexes with FK506 and rapamycin," *J Mol Biol.* 1993 Jan 5;229(1):105-24.
		White et al., "*Biosynthesis of salvage pathways of pyridine nucleotide coenzymes.*" Academic Press, New York; title page, publication page, and table of contents only, 13 pages (1982)
		Willison, "An essential gene (efg) located at 38.1 minutes on the Escherichia coli chromosome," *J Bacteriol.* 1992 Sep;174(17):5765-6.
		Willison et al., "The Escherichia coli efg gene and the Rhodobacter capsulatus adgA gene code for NH3-dependent NAD synthetase," *J Bacteriol.* 1994 Jun;176(11):3400-2.
		Wyckoff et al., eds., *Methods in Enzymology Vol. 114 - Diffraction Methods for Biological Macromolecules,* Academic Press, Orlando, FL; title page, publication page, and table of contents only, 5 pages (1985).
		Wyckoff et al., eds., *Methods in Enzymology Vol. 115. Diffraction Methods for Biological Macromolecules*, Academic Press, Orlando, FL; title page, publication page, and table of contents only, 4 pages (1985).
		Zalkin, "NAD synthetase," *Methods Enzymol.* 1985;*113*:297-302.

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